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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Re the application of: Hermann Bujard and
Manfred Gossen

Group Art Unit: 1631

Examiner:

Serial No.: 09/921,650

Filed: August 3, 2001

For: *TETRACYCLINE-INDUCIBLE
TRANSCRIPTIONAL INHIBITOR FUSION
PROTEINS (as amended)*

Attorney Docket No.: BBI-009C6CNDVCN

Commissioner for Patents
Box Sequence
Washington, D.C. 20231

**TRANSMITTAL LETTER FOR DISKETTE CONTAINING
SUBSTITUTE SEQUENCE LISTING**

Dear Sir:

Responsive to the Notice to File Missing Parts of NonProvisional Application, enclosed is a diskette which contains a computer readable form of the Substitute Sequence Listing filed for the above-identified patent application. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821. The material on this diskette is identical in substance to the sequence listing appearing on pages 75-101 of the Sequence Listing which is submitted herewith, as required by 37 C.F.R. §1.821(f). The computer readable form of the Substitute Sequence Listing contained on the enclosed diskette is understood to comply with the requirements of §1.824(d).

Certificate of First Class Mailing (37 CFR 1.8(a))

I hereby certify that this correspondence is deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Box Missing Parts, Washington, D.C. 20231 on:

3-26-02

Date

Giulio A. DeConti, Jr., Esq., Reg. No. 31,503

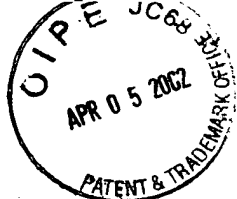
Respectfully submitted,

LAHIVE & COCKFIELD, LLP

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Reg. No. 31,503

Attorney for Applicants



SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Bujard, Hermann
Gossen, Manfred

10 (ii) TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
Inhibitor Fusion Proteins

10 (iii) NUMBER OF SEQUENCES: 37

15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LAHIVE & COCKFIELD
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20 (F) ZIP: 02109-1875

25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: ASCII Text

30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/921,650
(B) FILING DATE: 03-AUG-2001
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/489,777
(B) FILING DATE: 24-JAN-2000
(C) CLASSIFICATION:

40 (vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: US 09/162,184
(B) FILING DATE: 28-SEP-1998
(C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: US 08/485,978
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

50 (vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: US 08/383,754
(B) FILING DATE: 03-FEB-1995
(C) CLASSIFICATION:

55 (vii) PRIOR APPLICATION DATA
(A) APPLICATION NUMBER: US 08/275,876
(B) FILING DATE: 15-JULY-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA
 (A) APPLICATION NUMBER: US 08/270,637
 (B) FILING DATE: 01-JULY-1994
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA
 (A) APPLICATION NUMBER: US 08/260,452
 (B) FILING DATE: 14-JUNE-1994
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA
 (A) APPLICATION NUMBER: US 08/076,327
 (B) FILING DATE: 14-JUNE-1993
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA
 (A) APPLICATION NUMBER: US 08/076,726
 (B) FILING DATE: 14-JUNE-1993
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
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 (C) REFERENCE/DOCKET NUMBER: BBI-009C6CNDVCN

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1008 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 1..1008

(ix) FEATURE:
 (A) NAME/KEY: mRNA
 (B) LOCATION: 1..1008

(ix) FEATURE:
 (A) NAME/KEY: misc. binding
 (B) LOCATION: 1..207

(ix) FEATURE:
 (A) NAME/KEY: misc. binding
 (B) LOCATION: 208..335

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1005

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu	48
	1 5 10 15	
10	CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	96
	20 25 30	
15	AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	144
	35 40 45	
20	CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	192
	50 55 60	
25	ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg	240
	65 70 75 80	
30	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly	288
	85 90 95	
35	GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	336
	100 105 110	
40	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	384
	115 120 125	
45	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	432
	130 135 140	
50	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	480
	145 150 155 160	
55	CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	528
	165 170 175	
60	TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	576
	180 185 190	
65	ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala	624
	195 200 205	
70	TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly	672
	210 215 220	

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CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG 720
 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala 240
 225 230 235

5 GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG 768
 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser 255
 245 250

10 ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC 816
 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp 270
 260 265

15 GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT 864
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp 285
 275 280

20 CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 912
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro 300
 290 295

CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT 960
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe 320
 305 310 315

25 GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG 1008
 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly 335
 325 330

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

40 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30

45 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45

50 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50 55 60

Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80

55 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
 85 90 95

Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100 105 110

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Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
 115 120 125
 5 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
 130 135 140
 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
 145 150 155 160
 10 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 165 170 175
 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 180 185 190
 15 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
 195 200 205
 20 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
 210 215 220
 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
 225 230 235 240
 25 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
 245 250 255
 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
 260 265 270
 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
 275 280 285
 35 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 290 295 300
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 305 310 315 320
 40 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
 325 330 335

45 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG 33
 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Lys Arg Pro Arg Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG 60
 TGGATGGCGT CTCCAGGCGA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA 120

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5 GTTTACCACT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA 180
GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA 240
AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC 300
CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA 360
10 AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG 420
TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA 480
ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTTGA CCTCCATAGA AGACACCGGG 540
15 ACCGATCCAG CCTCCGCGGC CCCGAATTC 569

20 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGATCTGCAG GGTCGCTCGG TGTTGAGGC CACACGCGTC ACCTTAATAT GCGAAGTGGA 60
CCGGATCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 120
35 ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 180
AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 240
40 TTTACCACTC CCTATCAGTG ATAGAGAAAA GTGAAAGTCG AGTTTACCAC TCCCTATCAG 300
TGATAGAGAA AAGTGAAAGT CGAGTTTACC ACTCCCTATC AGTGATAGAG AAAAGTGAAA 360
GTCGAGCTCG GTACCCGGGT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 420
45 TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG 480
AAGACACCGG GACCGATCCA GCCTCCGCGG CCCC GAATTC 520

50 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human cytomegalovirus
(B) STRAIN: K12, Towne

(ix) FEATURE:

- (A) NAME/KEY: mRNA
(B) LOCATION: 382..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 60
ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 120
AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 180
TTTACCACTC CCTATCAGTG ATAGAGAAAA GTGAAAGTCG AGTTTACCAC TCCCTATCAG 240
TGATAGAGAA AAGTGAAAGT CGAGTTTACC ACTCCCTATC AGTGATAGAG AAAAGTGAAA 300
GTCGAGCTCG GTACCCGGGT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 360
TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG 420
AAGACACCGG GACCGATCCA GCCTCCGCGG 450

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human cytomegalovirus
(B) STRAIN: Towne

(ix) FEATURE:

- (A) NAME/KEY: mRNA
(B) LOCATION: 382..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCTCG ACCCGGGTAC CGAGCTCGAC TTCTACTTTT CTCTATCACT GATAGGGAGT 60
GGTAAACTCG ACTTTCACTT TTCTCTATCA CTGATAGGGA GTGGTAAACT CGACTTTCAC 120
TTTTCTCTAT CACTGATAGG GAGTGGTAAA CTCGACTTTC ACTTTTCTCT ATCACTGATA 180
GGGAGTGGTA AACTCGACTT TCACTTTTCT CTATCACTGA TAGGGAGTGG TAAACTCGAC 240
TTTCACTTTT CTCTATCACT GATAGGGAGT GGTAAACTCG ACTTTCACTT TTCTCTATCA 300

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CTGATAGGGA GTGGTAAACT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 360
TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG 420
AAGACACCGG GACCGATCCA GCCTCCGCGG 450

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Herpes Simplex Virus
- (B) STRAIN: KOS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCTCGACT TTCACITTTTC TCTATCACTG ATAGGGAGTG GTAAACTCGA CTTTCACTTT 60
TCTCTATCAC TGATAGGGAG TGGTAAACTC GACTTTCACT TTTCTCTATC ACTGATAGGG 120
AGTGGTAAAC TCGACTTTCA CTTTCTCTA TCACTGATAG GGAGTGGTAA ACTCGACTTT 180
CACTTTTCTC TATCACTGAT AGGGAGTGGT AACTCGACT TTCACITTTTC TCTATCACTG 240
ATAGGGAGTG GTAAACTCGA CTTTCACTTT TCTCTATCAC TGATAGGGAG TGGTAAACTC 300
GAGATCCGGC GAATTCGAAC ACGCAGATGC AGTCGGGGCG GCGCGGTCCG AGGTCCACTT 360
CGCATATTAA GGTGACGCGT GTGGCCTCGA ACACCGAG 398

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTTTATCAC TGATAAACAA ACTTATCAGT GATAAAGA

38

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACTCTATCAT TGATAGAGTT CCCTATCAGT GATAGAGA

38

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTATCAT CGATAAGCTA GTTTATCACA GTTAAATT

38

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCTATCAT TGATAGGGAA CTCTATCAAT GATAGGGA

38

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATCTATCAC TGATAGAGTA CCCTATCATC GATAGAGA

38

5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 621 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20

ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG	48
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu	
1 5 10 15	

25

CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG	96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
20 25 30	

30

AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG	144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
35 40 45	

CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT	192
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
50 55 60	

35

ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT	240
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg	
65 70 75 80	

40

AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA	288
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly	
85 90 95	

45

GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT	336
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
100 105 110	

50

CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG	384
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
115 120 125	

AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
130 135 140	

55

GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
145 150 155 160	

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CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528
 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 165 170 175

5 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG 576
 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 180 185 190

10 ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC 621
 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:17:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

25 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30

30 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45

35 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80

40 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
 85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100 105 110

45 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
 115 120 125

50 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
 130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
 145 150 155 160

55 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 180 185 190

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Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 621 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG	48
	Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu	
	1 5 10 15	
25	CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG	96
	Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
	20 25 30	
30	AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG	144
	Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
	35 40 45	
35	CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT	192
	Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
	50 55 60	
40	ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC	240
	Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg	
	65 70 75 80	
45	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA	288
	Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly	
	85 90 95	
50	GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT	336
	Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
	100 105 110	
55	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG	384
	Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
	115 120 125	
60	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432
	Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
	130 135 140	
65	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480
	Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
	145 150 155 160	

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CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA 528
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
165 170 175

5 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG 576
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
180 185 190

10 ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC 621
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
50 55 60

Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
85 90 95

Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
165 170 175

5 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:20:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20	GAC Asp 1	ATG Met	GAA Glu	AAA Lys	GCG Ala 5	ACA Thr	CCG Pro	GAG Glu	ACG Thr	ATG Met 10	GTC Val	CAT His	TGG Trp	ATT Ile 15	TGT Cys	CTG Leu	48
25	AAG Lys	ATG Met	GAG Glu	CCA Pro 20	GCT Ala	CTG Leu	TGG Trp	ATG Met	GCC Ala 25	ATT Ile	ACA Thr	GCA Ala	ACA Thr 30	TCG Ser	CAC His	GGC Gly	96
30	GCA Ala	AGG Arg 35	CAC His	AGG Arg	ACA Thr	TTC Phe	GTC Val	GGG Gly 40	TTT Phe	TCC Ser	GGC Gly	TGC Cys 45	CTC Leu	CAC His	CGC Arg	AAA Lys	144
35	TCC Ser 50	CTC Leu	ACG Thr	TAC Tyr	CCA Pro	GTG Val 55	ATA Ile	TGC Cys	CTG Leu	AGC Ser	AAA Lys 60	CCG Pro	AGC Ser	CAG Gln	AGG Arg	ATT Ile	192

(2) INFORMATION FOR SEQ ID NO:21:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

50  Asp Met Glu Lys Ala Thr Pro Glu Thr Met Val His Trp Ile Cys Leu
    1          5          10          15

    Lys Met Glu Pro Ala Leu Trp Met Ala Ile Thr Ala Thr Ser His Gly
          20          25          30

55  Ala Arg His Arg Thr Phe Val Gly Phe Ser Gly Cys Leu His Arg Lys
    35          40          45

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Ser Leu Thr Tyr Pro Val Ile Cys Leu Ser Lys Pro Ser Gln Arg Ile
 50 55 60

5 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTG GAC GAC TCG AAG CGC GTA GCC AAG CGG AAG CTG ATC GAG GAG AAC 48
 Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn
 20 1 5 10 15

CGG GAG CGG CGA CGC AAG GAG GAG ATG ATC AAA TCC CTG CAG CAC CGG 96
 Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg
 20 25 30

CCC AGC CCC AGC GCA GAG GAG TGG GAG CTG ATC CAC GTG GTG ACC GAG 144
 Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu
 35 40 45

GCG CAC CGC AGC ACC AAC GCG CAG GGC AGC CAC TGG AAG CAG AGG AGG 192
 Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg
 50 55 60

AAA TTC CTG CTC GAA GAT ATC GGT CAG TCG CCC ATG GCC TCC ATG CTT 240
 Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu
 65 70 75 80

GAC GGG GAC AAA GTG GAC CTG GAG GCG TTC AGC GAG TTT ACA AAA ATC 288
 Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile
 40 85 90 95

ATC ACG CCG GCC ATC ACC CGC GTG GTC GAC TTT GCC AAA AAC CTG CCC 336
 Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro
 100 105 110

ATG TTC TCG GAG CTG CCG TGC GAG GAT CAG ATC ATC CTG CTG AAG GGC 384
 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly
 115 120 125

TGC TGC ATG GAG ATC ATG TCG CTG CGC GCC GCC GTG CGC TAC GAC CCC 432
 Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro
 130 135 140

GAG AGC GAA ACG CTG ACG CTG AGC GGG GAA ATG GCC GTC AAA CGC GAG 480
 Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu
 145 150 155 160

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	CAG TTG AAG AAC GGA GGG CTG GGG GTC GTG TCT GAT GCC ATC TTC GAC	528
	Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp	
	165 170 175	
5	CTC GGC AAG TCG CTG TCT GCC TTC AAC CTG GAC GAC ACC GAG GTG GCC	576
	Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala	
	180 185 190	
10	CTG CTG CAG GCC GTG CTG CTC ATG TCC TCA GAC CGG ACG GGG CTG ATC	624
	Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile	
	195 200 205	
15	TGC GTG GAT AAG ATA GAG AAG TGC CAG GAG TCG TAC CTG CTG GCG TTC	672
	Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe	
	210 215 220	
20	GAG CAC TAC ATC AAC TAC CGC AAA CAC AAC ATT CCC CAC TTC TGG TCC	720
	Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser	
	225 230 235 240	
	AAG CTG CTG ATG AAG GTG GCG GAC CTG CGC ATG ATC GGC GCC TAC CAC	768
	Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His	
	245 250 255	
25	GCC AGC CGC TTC CTG CAC ATG AAG GTG GAG TGC CCC ACC GAG CTC TCC	816
	Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser	
	260 265 270	
30	(2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 272 amino acids	
	(B) TYPE: amino acid	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
	Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn	
	1 5 10 15	
45	Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg	
	20 25 30	
	Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu	
50	35 40 45	
	Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg	
	50 55 60	
55	Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu	
	65 70 75 80	
	Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile	
	85 90 95	

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Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro
100 105 110

5 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly
115 120 125

Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro
130 135 140

10 Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu
145 150 155 160

15 Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp
165 170 175

Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala
180 185 190

20 Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile
195 200 205

Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe
210 215 220

25 Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser
225 230 235 240

30 Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His
245 250 255

Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser
260 265 270

35 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCCCCGGGTA ACTAAGTAAG GATCC

25

50

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

5 AGTGGGTCCC CGGGTGACAT GGAA

24

(2) INFORMATION FOR SEQ ID NO:26:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: polypeptide
(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Gly Ser Pro Gly Asp Met Glu
1 5

25 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

40 AGTGGGTCCC CGGGTCTGGA CGAC

24

(2) INFORMATION FOR SEQ ID NO:28:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: polypeptide
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

55 Ser Gly Ser Pro Gly Leu Asp Asp
1 5

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50 55 60

Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80

Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
 85 90 95

Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
 115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
 130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
 145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

5 Met Ala Arg Leu Asn Arg Glu Ser Val Ile Asp Ala Ala Leu Gly Leu
 1 5 10 15
 Leu Asn Glu Thr Gly Ile Asp Glu Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30
 10 Lys Leu Gly Ile Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45
 Arg Ala Leu Leu Asp Ala Leu Ala Val Glu Ile Leu Ala Arg His His
 50 55 60
 15 Asp Tyr Ser Leu Pro Ala Ala Gly Glu Ser Trp Gln Ser Phe Leu Arg
 65 70 75 80
 20 Asn Asn Ala Met Ser Phe Arg Arg Ala Leu Leu Arg Tyr Arg Asp Gly
 85 90 95
 Ala Lys Val His Leu Gly Thr Arg Pro Asp Glu Lys Gln Tyr Asp Thr
 100 105 110
 25 Val Glu Thr Gln Leu Arg Phe Met Thr Glu Asn Gly Phe Ser Leu Arg
 115 120 125
 Asp Gly Leu Tyr Ala Ile Ser Ala Val Ser His Phe Thr Leu Gly Ala
 130 135 140
 30 Val Leu Glu Gln Gln Glu His Thr Ala Ala Leu Thr Asp Arg Pro Ala
 145 150 155 160
 35 Ala Pro Asp Glu Asn Leu Pro Pro Leu Leu Arg Glu Ala Leu Gln Ile
 165 170 175
 Met Asp Ser Asp Asp Gly Glu Gln Ala Phe Leu His Gly Leu Glu Ser
 180 185 190
 40 Leu Ile Arg Gly Phe Glu Val Gln Leu Thr Ala Leu Leu Gln Ile Val
 195 200 205
 Gly Gly Asp Lys Leu Ile Ile Pro Phe Cys
 210 215

(2) INFORMATION FOR SEQ ID NO:31:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Thr Lys Leu Gln Pro Asn Thr Val Ile Arg Ala Ala Leu Asp Leu
 1 5 10 15

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Leu Asn Glu Val Gly Val Asp Gly Leu Thr Thr Arg Lys Leu Ala Glu
 20 25 30
 5 Arg Leu Gly Val Gln Gln Pro Ala Leu Tyr Trp His Phe Arg Asn Lys
 35 40 45
 Arg Ala Leu Leu Asp Ala Leu Ala Glu Ala Met Leu Ala Glu Asn His
 50 55 60
 10 Thr His Ser Val Pro Arg Ala Asp Asp Asp Trp Arg Ser Phe Leu Ile
 65 70 75 80
 Gly Asn Ala Arg Ser Phe Arg Gln Ala Leu Leu Ala Tyr Arg Asp Gly
 85 90 95
 15 Ala Arg Ile His Ala Gly Thr Arg Pro Gly Ala Pro Gln Met Glu Thr
 100 105 110
 20 Ala Asp Ala Gln Leu Arg Phe Leu Cys Glu Ala Gly Phe Ser Ala Gly
 115 120 125
 Asp Ala Val Asn Ala Leu Met Thr Ile Ser Tyr Phe Thr Val Gly Ala
 130 135 140
 25 Val Leu Glu Glu Gln Ala Gly Asp Ser Glu Ser Gly Glu Arg Gly Gly
 145 150 155 160
 Thr Val Glu Gln Ala Pro Leu Ser Pro Leu Leu Arg Ala Ala Ile Asp
 165 170 175
 30 Ala Phe Asp Glu Ala Gly Pro Asp Ala Ala Phe Glu Gln Gly Leu Ala
 180 185 190
 35 Val Ile Val Asp Gly Leu Ala Lys Arg Arg Leu Val Val Arg Asn Val
 195 200 205
 Glu Gly Pro Arg Lys Gly Asp Asp
 210 215

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

55 Met Asn Lys Leu Gln Arg Glu Ala Val Ile Arg Thr Ala Leu Gly Leu
 1 5 10 15
 Leu Asn Asp Val Gly Met Glu Gly Leu Thr Thr Arg Arg Leu Ala Glu
 20 25 30

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Arg Leu Gly Val Gln Gln Pro Ala Leu Tyr Trp His Phe Lys Asn Lys
 35 40 45
 5 Arg Ala Leu Leu Asp Ala Leu Ala Glu Ala Met Leu Thr Ile Asn His
 50 55 60
 Thr His Ser Thr Pro Arg Asp Asp Asp Asp Trp Arg Ser Phe Leu Lys
 65 70 75 80
 10 Gly Asn Ala Cys Ser Phe Arg Arg Ala Leu Leu Ala Tyr Arg Asp Gly
 85 90 95
 Ala Arg Ile His Ala Gly Thr Arg Pro Ala Ala Pro Gln Met Glu Lys
 100 105 110
 15 Ala Asp Ala Gln Leu Arg Phe Leu Cys Asp Ala Gly Phe Ser Ala Gly
 115 120 125
 Asp Ala Thr Tyr Ala Leu Met Ala Ile Ser Tyr Phe Thr Val Gly Ala
 130 135 140
 Val Leu Glu Gln Gln Ala Ser Glu Ala Asp Ala Glu Glu Arg Gly Glu
 145 150 155 160
 25 Asp Gln Leu Thr Thr Ser Ala Ser Thr Met Pro Ala Arg Leu Gln Ser
 165 170 175
 Ala Met Lys Ile Val Tyr Glu Ala Gly Pro Asp Ala Ala Phe Glu Arg
 180 185 190
 30 Gly Leu Ala Leu Ile Ile Gly Gly Leu Glu Lys Met Arg Leu Thr Thr
 195 200 205
 Asn Asp Ile Glu Val Leu Lys Asn Val Asp Glu
 35 210 215

(2) INFORMATION FOR SEQ ID NO:33:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50 Met Thr Lys Leu Asp Lys Gly Thr Val Ile Ala Ala Gly Leu Glu Leu
 1 5 10 15
 Leu Asn Glu Val Gly Met Asp Ser Leu Thr Thr Arg Lys Leu Ala Glu
 20 25 30
 55 Arg Leu Lys Val Gln Gln Pro Ala Leu Tyr Trp His Phe Gln Asn Lys
 35 40 45
 Arg Ala Leu Leu Asp Ala Leu Pro Glu Ala Met Leu Arg Glu Arg His
 50 55 60

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Thr Arg Ser Leu Pro Glu Glu Asn Glu Asp Trp Arg Val Phe Leu Lys
 65 70 75 80
 5 Glu Asn Ala Leu Ser Phe Arg Thr Ala Leu Leu Ser Tyr Arg Asp Gly
 85 90 95
 Ala Arg Ile His Ala Gly Thr Arg Pro Thr Glu Pro Asn Phe Gly Thr
 100 105 110
 10 Ala Glu Thr Gln Ile Arg Phe Leu Cys Ala Glu Gly Phe Cys Pro Lys
 115 120 125
 Arg Ala Val Trp Ala Leu Arg Ala Val Ser His Tyr Val Val Gly Ser
 130 135 140
 15 Val Leu Glu Gln Gln Ala Ser Asp Ala Asp Glu Arg Val Pro Asp Arg
 145 150 155 160
 20 Pro Asp Val Ser Glu Gln Ala Pro Ser Ser Phe Leu His Val Leu Phe
 165 170 175
 His Glu Leu Glu Thr Asp Gly Met Asp Ala Ala Phe Asn Phe Gly Leu
 180 185 190
 25 Asp Ser Leu Ile Ala Gly Phe Glu Arg Leu Arg Ala Ala Val Leu Ala
 195 200 205
 30 Thr Asp
 210

(2) INFORMATION FOR SEQ ID NO:34:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

45 Met Ala Arg Leu Ser Leu Asp Asp Val Ile Ser Met Ala Leu Thr Leu
 1 5 10 15
 Leu Asp Ser Glu Gly Leu Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30
 50 Ser Leu Lys Ile Glu Gln Pro Thr Leu Tyr Trp His Val Arg Asn Lys
 35 40 45
 Gln Thr Leu Met Asn Met Leu Ser Glu Ala Ile Leu Ala Lys His His
 50 55 60
 55 Thr Arg Ser Ala Pro Leu Pro Thr Glu Ser Trp Gln Gln Phe Leu Gln
 65 70 75 80

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Glu Asn Ala Leu Ser Phe Arg Lys Ala Leu Leu Val His Arg Asp Gly
 85 90 95
 5 Ala Arg Leu His Ile Gly Thr Ser Pro Thr Pro Pro Gln Phe Glu Gln
 100 105 110
 Ala Glu Ala Gln Leu Arg Cys Leu Cys Asp Ala Gly Phe Ser Val Glu
 115 120 125
 10 Glu Ala Leu Phe Ile Leu Gln Ser Ile Ser His Phe Thr Leu Gly Ala
 130 135 140
 Val Leu Glu Glu Gln Ala Thr Asn Gln Ile Glu Asn Asn His Val Ile
 145 150 155 160
 15 Asp Ala Ala Pro Pro Leu Leu Gln Glu Ala Phe Asn Ile Gln Ala Arg
 165 170 175
 20 Thr Ser Ala Glu Met Ala Phe His Phe Gly Leu Lys Ser Leu Ile Phe
 180 185 190
 Gly Phe Ser Ala Gln Leu Asp Glu Lys Lys His Thr Pro Ile Glu Asp
 195 200 205
 25 Gly Asn Lys
 210

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

agttctatgt ctagattaga taaaagtaaa gtgattaaca gcgcattaga gctgcttaat 60
 gaggtcggaa tcgaaggttt aacaaccggt aaactcgccc agaagctagg tgtagagcag 120
 45 cctacattgt attggcatgt aaaaaataag cgggctttgc tcgacgcctt agccattgag 180
 atgttagata ggcaccatac tactttttgc ctttagaag gggaaagctg gcaagatttt 240
 50 ttacgtaata aggctaaaag ttttagatgt gctttactaa gtcacgcga tggagcaaaa 300
 gtacatttag gtacacggcc tacagaaaaa cagtatgaaa ctctcgaaaa tcaattagcc 360
 55 tttttatgcc aacaaggttt ttcactagag aatgcattat atgcactcag cgctgtgggg 420
 cattttactt taggttgcgt attggaagat caagagcatc aagtcgctaa agaagaaagg 480
 gaaacaccta ctactgatag tatgccgcca ttattacgac aagctatcga attatttgat 540

- 100 -

caccaaggtg cagagccagc cttcttattc ggccttgaat tgatcatatg cggattagaa 600
aaacaactta aatgtgaaag tgggtccgac atggaaaaag cgacaccgga gacgatggtc 660
5 cattggattt gtctgaagat ggagccagct ctgtggatgg ccattacagc aacatcgac 720
ggcgcaaggc acaggacatt cgtcgggttt tccggctgcc tccaccgcaa atccctcacg 780
taccagtgat tatgcctgag caaacgagc cagaggatt 819

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

atgtctatgt ctagattaga taaaagtaaa gtgattaaca ggcattaga gctgcttaat 60
gaggtcggaa tcgaaggttt aacaaccgt aaactcgccc agaagctagg ttagagcag 120
cctacattgt attggcatgt aaaaaataag cgggctttgc tcgacgcctt agccattgag 180
atgttagata ggcaccatac tcacttttgc cctttagaag gggaaagctg gcaagatttt 240
ttacgtaata aggctaaaag ttttagatgt gctttactaa gtcacgcga tggagcaaaa 300
gtacatttag gtacacggcc tacagaaaaa cagtatgaaa ctctcgaaaa tcaattagcc 360
tttttatgcc aacaaggttt ttactagag aatgcattat atgcactcag cgctgtgggg 420
cattttactt taggttgctg attggaagat caagagcatc aagtcgctaa agaagaaagg 480
gaaacaccta ctactgatag tatgccgcca ttattacgac aagctatcga attatttgat 540
caccaaggtg cagagccagc cttcttattc ggccttgaat tgatcatatg cggattagaa 600
45 aaacaactta aatgtgaaag tgggtcctcc ccgggtaact aagtaaggat cc 652

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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atgtctatgt ctagattaga taaaagtaaa gtgattaaca gcgcattaga gctgcttaat 60
5 gaggtcggaa tcgaagggtt aacaacccgt aaactcgccc agaagctagg tgtagagcag 120
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atgttagata ggcaccatac tcacttttgc cctttagaag gggaaagctg gcaagatttt 240
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50 tcc

1443